

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/933,115A

CRF Processing Date: 2/11/2002
 Edited by: [Signature]
 Verified by: [Signature] (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____



OIPE

RAW SEQUENCE LISTING

DATE: 02/11/2002

PATENT APPLICATION: US/09/933,115A

TIME: 18:07:35

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\02112002\I933115A.raw

PS

```

4 <110> APPLICANT: Fisher, Paul B.
6 <120> TITLE OF INVENTION: COMBINATORIAL METHODS FOR INDUCING
7   CANCER CELL DEATH
9 <130> FILE REFERENCE: A34466 070050.1618
11 <140> CURRENT APPLICATION NUMBER: US 09/933,115A
12 <141> CURRENT FILING DATE: 2001-08-20
14 <160> NUMBER OF SEQ ID NOS: 17
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1700
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: misc_feature
25 <222> LOCATION: (275)...(895)
26 <223> OTHER INFORMATION: CDS = 275-895
28 <400> SEQUENCE: 1
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30 cacagctatg cctctgattg gtgaatgggtg aagggtgcctg tctaactttt ctgtaaaaag 120
31 aaccagctgc ctccaggcag ccagccctca agcatcactt acaggaccag agggacaaga 180
32 catgactgtg atgaggagct gctttcgcca atttaacacc aagaagaatt gaggctgctt 240
33 gggagggaagg ccaggaggaa cacgagactg agagatgaat tttcaacaga ggctgcaaag 300
34 cctgtggact ttagccagac ccttctgccc tcctttgctg gcgacagcct ctcaaatgca 360
35 gatggttggtg ctcccttgcc tgggttttac cctgcttctc tggagccagg tatcaggggc 420
36 ccagggccaa gaattccact ttggggccctg ccaagtgaag ggggttggtc ccagaaaact 480
37 gtgggaagcc ttctgggctg tgaaagacac tatgcaagct caggataaca tcacgagtgc 540
38 ccggctgctg cagcaggagg ttctgcagaa cgtctcggat gctgagagct gttacctgtg 600
39 ccacaccctg ctggagttct acttgaaaac tgttttcaaa aactaccaca atagaacagt 660
40 tgaagtcagg actctgaagt cattctctac tctggccaac aactttgttc tcatcgtgtc 720
41 acaactgcaa ccagtcgaag aaaatgagat gttttccatc agagacagtg cacacaggcg 780
42 gttttctgcta ttccggagag cattcaaaca gttggacgta gaagcagctc tgaccaaaagc 840
43 ccttggggaa gtggacattc ttctgacctg gatgcagaaa ttctacaagc tctgaatgtc 900
44 tagaccagga cctccctccc cctggcactg gtttgttccc tgtgtcattt caaacagtct 960
45 cccttcctat gctgttcaact ggacacttca cgccttggc catgggtccc attcttgccc 1020
46 caggattatt gtcaaagaag tcattcttta agcagcgcca gtgacagtca gggaagggtgc 1080
47 ctctggatgc tgtgaagagt ctacagagaa gattcttgta tttattacaa ctctatttaa 1140
48 ttaatgtcag tatttcaact gaagtcttat ttatttgta gactgtaagt tacatgaagg 1200
49 cagcagaata ttgtgcccc a tgcttcttta cccctcacia tccttgccac agtgtggggc 1260
50 agtgggatggg tgcttagtaa gtacttaata aactgtgggtg ctttttttgg cctgtctttg 1320
51 gattgttaaa aaacagagag ggatgcttgg atgtaaaact gaacttcaga gcatgaaaat 1380
52 cacactgtct gctgatatct gcagggacag agcattgggg tgggggtaag gtgcatctgt 1440
53 ttgaaaagta aacgataaaa tgtggattaa agtgcccagc acaaagcaga tcctcaataa 1500
54 acatttcatt tcccaccac actcgccagc tcaccccatc atccctttcc cttggtgccc 1560

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55 tcctttttttt tttatcctag tcattcttcc ctaatcttcc acttgagtgt caagctgacc 1620
56 ttgctgatgg tgacattgca cctggatgta ctatccaatc tgtgatgaca ttccctgcta 1680
57 ataaaagaca acataactca                                     1700
59 <210> SEQ ID NO: 2
60 <211> LENGTH: 206
61 <212> TYPE: PRT
62 <213> ORGANISM: Homo sapiens
64 <400> SEQUENCE: 2
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66 1 5 10 15
67 Phe Cys Pro Pro Leu Leu Ala Thr Ala Ser Gln Met Gln Met Val Val
68 20 25 30
69 Leu Pro Cys Leu Gly Phe Thr Leu Leu Leu Trp Ser Gln Val Ser Gly
70 35 40 45
71 Ala Gln Gly Gln Glu Phe His Phe Gly Pro Cys Gln Val Lys Gly Val
72 50 55 60
73 Val Pro Gln Lys Leu Trp Glu Ala Phe Trp Ala Val Lys Asp Thr Met
74 65 70 75 80
75 Gln Ala Gln Asp Asn Ile Thr Ser Ala Arg Leu Leu Gln Gln Glu Val
76 85 90 95
77 Leu Gln Asn Val Ser Asp Ala Glu Ser Cys Tyr Leu Val His Thr Leu
78 100 105 110
79 Leu Glu Phe Tyr Leu Lys Thr Val Phe Lys Asn Tyr His Asn Arg Thr
80 115 120 125
81 Val Glu Val Arg Thr Leu Lys Ser Phe Ser Thr Leu Ala Asn Asn Phe
82 130 135 140
83 Val Leu Ile Val Ser Gln Leu Gln Pro Ser Gln Glu Asn Glu Met Phe
84 145 150 155 160
85 Ser Ile Arg Asp Ser Ala His Arg Arg Phe Leu Leu Phe Arg Arg Ala
86 165 170 175
87 Phe Lys Gln Leu Asp Val Glu Ala Ala Leu Thr Lys Ala Leu Gly Glu
88 180 185 190
89 Val Asp Ile Leu Leu Thr Trp Met Gln Lys Phe Tyr Lys Leu
90 195 200 205
93 <210> SEQ ID NO: 3
94 <211> LENGTH: 20
95 <212> TYPE: DNA
96 <213> ORGANISM: Homo sapiens
98 <220> FEATURE:
99 <221> NAME/KEY: misc_feature
100 <222> LOCATION: (0)...(0)
101 <223> OTHER INFORMATION: primer for mda-7
103 <400> SEQUENCE: 3
104 atgctctgtc cctgcagata                                     20
106 <210> SEQ ID NO: 4
107 <211> LENGTH: 20
108 <212> TYPE: DNA
109 <213> ORGANISM: Homo sapiens
111 <220> FEATURE:

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112 <221> NAME/KEY: misc_feature
113 <222> LOCATION: (0)...(0)
114 <223> OTHER INFORMATION: primer for MDA-7
116 <400> SEQUENCE: 4
117 ctctggatgc tgtgaagagt 20
119 <210> SEQ ID NO: 5
120 <211> LENGTH: 12
121 <212> TYPE: PRT
122 <213> ORGANISM: Homo sapiens
124 <220> FEATURE:
125 <223> OTHER INFORMATION: 153-164 of human MDA-7
127 <400> SEQUENCE: 5
128 Pro Ser Gln Glu Asn Glu Met Phe Ser Ile Arg Asp
129 1 5 10
132 <210> SEQ ID NO: 6
133 <211> LENGTH: 5775
134 <212> TYPE: DNA
135 <213> ORGANISM: Homo sapiens
137 <220> FEATURE:
138 <221> NAME/KEY: misc_feature
139 <222> LOCATION: (193)...(759)
140 <223> OTHER INFORMATION: CDS = 193-759
142 <400> SEQUENCE: 6
143 tcctaggcgg cggccgcggc ggcggaggca gcagcggcgg cggcagtggc ggcggcgaag 60
144 gtggcggcgg ctccggccagt actcccggcc cccgccattt cggactggga gcgagcgcgg 120
145 cgcaggcact gaaggcggcg gcggggccag aggcctcagc gctcccaggc gcgggagaga 180
146 ggcctgctga aaatgactga atataaacct gtggtagtgt gagcttgttg cgtaggcaag 240
147 agtgccttga cgatacagct aattcagaat cattttgttg acgaatatga tccaacaata 300
148 gaggattcct acaggaagca agtagtaatt gatggagaaa cctgtctctt ggatattctc 360
149 gacacagcag gtcaagagga gtacagtgcg atgagggacc agtacatgag gactggggag 420
150 ggctttcttt gtgtatttgc cataaataat actaaatcat ttgaagatat tcaccattat 480
151 agagaacaaa ttaaaagagt taaggactct gaagatgtac ctatggtcct agtaggaaat 540
152 aaatgtgatt tgccttctag aacagtagac acaaaacagg ctccaggact agcaagaagt 600
153 tatggaattc cttttattga aacatcagca aagacaagac aggggtgttg tgatgccttc 660
154 tatacattag ttcgagaaat tcgaaaacat aaagaaaaga tgagcaaaga tggtaaaaag 720
155 aagaaaaaga agtcaaagac aaagtgtgta attatgtaaa tacaatttgt acttttttct 780
156 taaggcatac tagtacaagt ggtaattttt gtacattaca ctaaattatt agcatttgtt 840
157 ttagcattac ctaatttttt tcctgtctcc tgcagactgt tagcttttac cttaaattgt 900
158 tattttaaaa tgacagtgga agtttttttt tcctcgaagt gccagtattc ccagagtttt 960
159 ggtttttgaa ctagcaatgc ctgtgaaaaa gaaactgaat acctaagatt tctgtcttgg 1020
160 ggtttttggt gcatgcagtt gattacttct tatttttctt accaagtgtg aatgttggtg 1080
161 tgaaacaaat taatgaagct tttgaatcat ccctattctg tgttttatct agtcacataa 1140
162 atggattaat tactaatttc agttgagacc ttctaattgg tttttactga aacattgagg 1200
163 catcaaaatt tatgggcttc ctgatgatga ttcttctagg catcatgtcc tatagtttgt 1260
164 catccctgat gaatgtaaaag ttacactgtt cacaaagggt ttgtctcctt tccactgcta 1320
165 ttagtcatgg tcaactctcc caaaatatta tattttttct ataaaaagaa aaaaatggaa 1380
166 aaaaattaca aggcaatgga aactattata aggccatttc cttttcacat tagataaatt 1440
167 actataaaga ctccataatg ctttttctct ttaaggcaga cccagtatga atgggattat 1500
168 tatagcaacc attttggggc tatatttaca tgctactaaa tttttataat aattgaaaag 1560

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169 attttaacaa gtataaaaaa attctcatag gaattaaatg tagtctccct gtgtcagact 1620
170 gctctttcat agtataaactt taaatctttt cttcaacttg agtctttgaa gatagtttta 1680
171 attctgcttg tgacattaaa agattatttg ggccagttat agcttattag gtgttgaaga 1740
172 gaccaagggt gcaagccagg ccctgtgtga accttgagct ttcatagaga gtttcacagc 1800
173 atggactgtg tgccccacgg tcatccgagt ggtgtacga tgcattggtt agtcaaaaaa 1860
174 ggggagggac tagggcagtt tggatagctc aacaagatac aatctcactc tgtggtggtc 1920
175 ctgctgacaa atcaagagca ttgcttttgt ttcttaagaa aacaaactct tttttaaaaa 1980
176 ttacttttaa atattaaactc aaaagttagg attttgggtt ggtggtgtgc caagacatta 2040
177 attttttttt taaacaatga agtgaaaaag ttttacaatc tctaggtttg gctagtcttc 2100
178 ttaacactgg ttaaaattaac attgcataaa cacttttcaa gtctgatcca tatttaataa 2160
179 tgctttaaaa taaaaataaa aacaatcctt ttgataaatt taaaatgtta cttattttta 2220
180 aataaatgaa gtgagatggc atggtgaggt gaaagtatca ctggactagg ttgttggtga 2280
181 cttaggttct agatagggtt cttttaggac tctgattttg aggacatcac ttactatcca 2340
182 tttcttcatg ttaaaagaag tcatctcaaa ctcttagttt ttttttttta cactatgtga 2400
183 tttatattcc atttacataa ggatacactt atttgcraag ctgagcacia tctgtaaatt 2460
184 tttaacctat gttacaccat cttcagtgcc agtcttgggc aaaattgtgc aagaggtgaa 2520
185 gtttatattt gaatatccat tctcgtttta ggactcttct tccatattag tgtcatcttg 2580
186 cctcctacc ttccacatgc ccatgactt gatgcagttt taatacttgt aattccccta 2640
187 accataagat ttactgctgc tgtggatctc tccatgaagt tttcccactg agtcacatca 2700
188 gaaatgccct acatcttatt ttctcaggg ctcaagagaa tctgacagat accataaagg 2760
189 gatttgacct aatcactaat tttcaggttg tggctgatgc tttgaacatc tctttgctgc 2820
190 ccaatccatt agcgacagta ggatttttca accctggtat gaatagacag aacctatcc 2880
191 agtggaagga gaatttaata aagatagtgc agaaagaatt ccttaggtaa tctataacta 2940
192 ggactactcc tggtaacagt aatacattcc attgttttag taaccagaaa tcttcatgca 3000
193 atgaaaaata ctttaattca tgaagcttac tttttttttt ttggtgtcag agtctcgctc 3060
194 ttgtcaccca ggctggaatg cagtggcgc atctcagctc actgcaacct tccatcttcc 3120
195 caggttcaag cgattctcgt gcttcggcct cctgagtagc tgggattaca ggcgtgtgca 3180
196 ctacactcaa ctaatttttg tatttttagg agagacggg tttcacctgt tggccaggct 3240
197 ggtctcgaac tctgacctc aagtgattca cccaccttg cctcataaac ctgttttgca 3300
198 gaaactattt attcagcaaa tatttattga gtgcctacca gatgccagtc accgcacaag 3360
199 gcactgggta tatggtatcc ccaaacaaga gacataatcc cggtccttag gtactgctag 3420
200 tgtggtctgt aatatcttac taaggccttt ggtatacgac ccagagataa cacgatgcgt 3480
201 attttagttt tgcaaagaag gggtttggtc tctgtgccag ctctataatt gttttgctac 3540
202 gattccactg aaactcttcg atcaagctac tttatgtaaa tcaattcatt gttttaagg 3600
203 aataaacttg atttatattg ttttttattt ggcataactg tgattctttt aggacaatta 3660
204 ctgtacacat taaggtgtat gtcagatatt catattgacc caaatgtgta atattccagt 3720
205 tttctctgca taagtaatta aaatatactt aaaaattaat agttttatct gggtaaaaat 3780
206 aaacagtgcc tgaactagtt cacagacaag ggaaacttct atgtaaaaat cactatgatt 3840
207 tctgaattgc tatgtgaaac tacagatctt tggaaactg tttaggtagg gtgttaagac 3900
208 ttgacacagt acctcgtttc tacacagaga aagaaatggc catacttcag gaactgcagt 3960
209 gcttatgagg ggatatttag gcctcttgaa tttttgatgt agatggcat ttttttaagg 4020
210 tagtggttaa ttacctttat gtgaactttg aatggtttta caaaagattt gttttttag 4080
211 agatttttaa gggggagaat tctagaaata aatgttacct aattattaca gccttaaga 4140
212 caaaaatcct tgttgaagtt tttttaaaaa aagactaaat tacatagact taggcattaa 4200
213 catgtttgtg gaagaatata gcagacgtat attgtatcat ttgagtgaat gttcccaagt 4260
214 aggcattcta ggctctattt aactgagtca cactgcatag gaatttagaa cctaactttt 4320
215 ataggttatc aaaactgttg tcaccattgc acaattttgt cctaataatat acatagaaac 4380
216 tttgtggggc atgttaagtt acagtttgca caagttcatc tcatttgat tccattgatt 4440
217 tttttttttc ttctaacaat tttttcttca aaacagtata tataactttt tttaggggat 4500

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218 ttttttttaga cagcaaaaaa ctatctgaag atttccattt gtcaaaaagt aatgatttct 4560
219 tgataattgt gtagtgaatg ttttttagaa cccagcagtt accttgaaaag ctgaatttat 4620
220 atttagtaac ttctgtgtta atactggata gcatgaattc tgcattgaga aactgaatag 4680
221 ctgtcataaa atgcttttctt tcctaaagaa agatactcac atgagttctt gaagaatagt 4740
222 cataactaga ttaagatctg tgtttttagtt taatagtttg aagtgcctgt ttgggataat 4800
223 gataggtaat ttagatgaat ttaggggaaa aaaaagttaa ctgcagttat gttgagggcc 4860
224 catctctccc cccacacccc cacagagcta actgggttac agtgttttat ccgaaagttt 4920
225 ccaattccac tgtcttgtgt ttcatgttg aaaatacttt tgcatttttc ctttgagtgc 4980
226 caatttctta ctagtactat ttcttaatgt aacatgttta cctggcctgt cttttaacta 5040
227 tttttgtata gtgtaaaactg aaacatgcac attttgtaca ttgtgctttc tttgtgggt 5100
228 cataatgcagt gtgatccagt tgttttccat catttggttg cgctgacctt ggaatgttgg 5160
229 tcatatcaaaa cattaaaaat gaccactctt ttaatgaaat taacttttaa atgtttatag 5220
230 gagtatgtgc tgtgaagtga tctaaaattt gtaatatatt tgtcatgaac tgtactactc 5280
231 ctaattattg taatgtaata aaaatagtta cagtactat gagtgtgtat ttattcatgc 5340
232 aaatttgaac tgtttgcccc gaaatggata tggatacttt ataagccata gacactatag 5400
233 tataaccagt aatcttttat gcagcttggtt agaagtatcc ttttattttc taaaaggtgc 5460
234 tgtggatatt atgtaaaggc gtgtttgctt aaacaatttt ccatatttag aagtagatgc 5520
235 aaaacaaatc tgcctttatg acaaaaaaat aggataacat tattttattt tttcctttta 5580
236 tcaataaggt aattgataca caacagggtga cttggtttta ggcccaaagg tagcagcagc 5640
237 aacattaata atggaaataa ttgaatagtt agttatgtat gttaatgcca gtcaccagca 5700
238 ggctatttca aggtcagaag taatgactcc atacatatta tttatttcta taactacatt 5760
239 taaatcatta ccagg 5775
241 <210> SEQ ID NO: 7
242 <211> LENGTH: 188
243 <212> TYPE: PRT
244 <213> ORGANISM: Homo sapiens
246 <400> SEQUENCE: 7
247 Met Thr Glu Tyr Leu Val Val Val Gly Ala Cys Gly Val Gly Lys
248 1 5 10 15
249 Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
250 20 25 30
251 Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
252 35 40 45
253 Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
254 50 55 60
255 Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
256 65 70 75 80
257 Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr
258 85 90 95
259 Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Glu Asp Val Pro Met Val
260 100 105 110
261 Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
262 115 120 125
263 Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
264 130 135 140
265 Ser Ala Lys Thr Arg Gln Gly Val Asp Asp Ala Phe Tyr Thr Leu Val
266 145 150 155 160
267 Arg Glu Ile Arg Lys His Lys Glu Lys Met Ser Lys Asp Gly Lys Lys
268 165 170 175

```

→ Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:279 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:316 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:353 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:390 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11